REMARKS

Claims 1-20 have been canceled without prejudice to or disclaimer of the subject matter recited therein.

Claims 21-31 are now pending, with Claim 21 being the sole independent claim.

Claims 21-31 have been added. Support for these claims are found throughout the specification, and at least at page 3, line 24; and Example 4. No new matter has been added.

The amendments to the specification merely correct clerical errors and remove hyperlinks to the world wide web. These changes are not believed to add any new matter to the application.

RESPONSE TO RESTRICTION REQUIREMENT

In the Office Action, Claims 1-20 were subject to restriction and/or election requirement. Applicants hereby elect Group I and the nucleic acid sequence of SEQ ID NO:8 encoding the polypeptide of SEQ ID NO:9 without traverse.

Pending claims 21-31 are directed to the elected invention of Group I and SEQ ID NO:9.

Please charge any requisite fees or credit any overpayment to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

In view of the foregoing, allowance of the application is earnestly solicited.

Respectfully submitted,

J. KENNETH JOUNG
ATTORNEY FOR APPLICANTS
REGISTRATION NO. 41,881
TELEPHONE: (302) 992-4929
FACSIMILE: (302) 892-1026

Dated: 19 February 2003

MARKED-UP VERSION SHOWING CHANGES MADE

In showing changes made, deletions are shown in [~~brackets with strikethrough~~], and additions are underlined.

IN THE SPECIFICATION:

Paragraph at page 3, lines 19-26:

It is preferred that the isolated polynucleotides of the claimed invention consist of a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 8, 11, 13, and 15 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 9, 12, 14, and 16. The present invention also relates to an isolated polynucleotide comprising a nucleotide sequences of at least [~~one of~~]40 (preferably at least [~~one of~~]30) contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 8, 11, 13, 15, and the complement of such nucleotide sequences.

Paragraph at page 4, lines 18-28:

The present invention relates to a method of obtaining a nucleic acid fragment encoding a substantial portion of a alpha toxin XIV, a neurotoxin I, or a depressant toxin LqhIT2 polypeptide gene, preferably a scorpion alpha toxin XIV, a neurotoxin I, or a depressant toxin LqhIT2 polypeptide gene, comprising the steps of: synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 40 (preferably at least [~~one of~~]30) contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 8, 11, 13, 15, and the complement of such nucleotide sequences; and amplifying a nucleic acid fragment (preferably a cDNA inserted in a cloning vector) using the oligonucleotide primer. The amplified nucleic acid fragment preferably will encode a portion of an alpha toxin XIV, a neurotoxin I, or a depressant toxin LqhIT2 amino acid sequence.

Paragraph at page 6, lines 11-19:

In the context of this disclosure, a number of terms shall be utilized. As used herein, a "polynucleotide" is a nucleotide sequence such as a nucleic acid fragment. A polynucleotide may be a polymer of RNA or DNA that is single- or double-stranded, that optionally contains synthetic, non-natural or altered nucleotide bases. A polynucleotide in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA, or synthetic DNA. An isolated polynucleotide of the present invention may include at least [~~one of~~]40 contiguous nucleotides, preferably at least [~~one of~~]30 contiguous nucleotides, most preferably [one of]at

least 15 contiguous nucleotides, of the nucleic acid sequence of the SEQ ID NOs:1, 3, 5, 8, 11, 13 and 15.

Paragraph at page 7, line 35 through page 8, line 19:

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410[~~; see also www.ncbi.nlm.nih.gov/BLAST/~~]). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

Paragraph at page 17, lines 8-24:

ESTs encoding scorpion sodium channel agonists were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410[~~; see also www.ncbi.nlm.nih.gov/BLAST/~~]) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National

Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet. 3*:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.